

FIG. 1A

1 CCCACGCGTCCGGGAGCTTGCCTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC 60
 61 CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTTATAAATAAATTTGCTC 120
 121 TTTCACCTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA 180
 181 GAGGCAGCAGAAGCCAGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG 240
 241 CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC 300
 301 TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT 360
 361 AAGGGAAAACTAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT 420
 421 GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAACGAGCATGGAGAGAAAAATT 480
 481 TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA 540
 1 M E P N G T F S N 9
 541 TAACAACAGCAGGAACTGCACAATTGAAAACCTCAAGAGAGAATTTTCCCAATTGTATA 600
 10 N N S R N C T I E N F K R E F F P I V Y 29
 601 TCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTCTGCA 660
 30 L I I F F W G V L G N G L S I Y V F L Q 49
 661 GCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTTCAGATCT 720
 50 P Y K K S T S V N V F M L N L A I S D L 69
 721 CCTGTTTATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT 780
 70 L F I S T L P F R A D Y Y L R G S N W I 89
 781 ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAG 840
 90 F G D L A C R I M S Y S L Y V N M Y S S 109
 841 TATTTATTTCTGACCGTGCTGAGTGTGTGCGTTTCTGGCAATGGTTCACCCCTTTTCG 900
 110 I Y F L T V L S V V R F L A M V H P F R 129

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FIG. 1B

901 GCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCT 960
 130 L L H V T S I R S A W I L C G I I W I L 149
 961 TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTAC 1020
 150 I M A S S I M L L D S G S E Q N G S V T 169
 1021 ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACATATATTGC 1080
 170 S C L E L N L Y K I A K L Q T M N Y I A 189
 1081 CTTGGTGGTGGGCTGCCTGCTGCCATTTTCACACTCAGCATCTGTTATCTGCTGATCAT 1140
 190 L V V G C L L P F F T L S I C Y L L I I 209
 1141 TCGGGTTCTGTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGC 1200
 210 R V L L K V E V P E S G L R V S H R K A 229
 1201 ACTGACCACCATCATCATCACCTTGATCATCTTCTTCTGTGTTTCTGCCCCTATCACAC 1260
 230 L T T I I I T L I I F F L C F L P Y H T 249
 1261 ACTGAGGACCGTCCACTTGACGACATGGAAGTGGGTTTATGCAAAGACAGACTGCATAA 1320
 250 L R T V H L T T W K V G L C K D R L H K 269
 1321 AGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTA 1380
 270 A L V I T L A L A A N A C F N P L L Y 289
 1381 TTACTTTGCTGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC 1440
 290 Y F A G E N F K D R L K S A L R K G H P 309
 1441 ACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAG 1500
 310 Q K A K T K C V F P V S V W L R K E T R 329
 1501 AGTATAAGGAGCTCTTAGATGAGACCTGTTCTTGTATCCTTGTGTCCATCTTCATTCAC 1560
 330 V * 331
 1561 CATAGTCTCCAAATGACTTTGTATTTACATCACTCCCAACAAATGTTGATTCTTAATATT 1620
 1621 TAGTTGACCATTACTTTTGTAAATAAGACCTACTTCAAAAATTTTATTAGTGTAACAAA 1680
 1681 AAAAAAAAAAAAAAAAAAAAAAAAAA 1708

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FIG. 2A

	1	50
HGPRBMY11	(1) -----MSLQPSISVSEEPNG-----TFNNMSRNCEN--FI	
HGPRBMY11v1	(1) MERKFMSLQPSISVSEEPNG-----TFNNMSRNCEN--FI	
P2Y5_CHICK	(1) -----MSSNC--TED--FI	
P2YR_CHICK	(1) MTEALISAALNGQPELAGG-----WAGNATKCKTKTGF	
P2YR_MELGA	(1) MTEALISAALNGQPELAGG-----WAGNATKCKTKTGF	
P2YR_RAT	(1) MTEVPWSAVPNGDAAGLAGLGSWGNSTIASAVSSFRCKTKTGF	
Q9Y271	(1) -----MDETG-----NLTVSSATCHDTIDDF	
GPRH_HUMAN	(1) -----MNGLEVAPPG-----LITNFSLVIAEQGQETP	
	51	100
HGPRBMY11	(22) REEPIVYILVFWCVLGNCSIVFQOPYKKSPEVNMENLAHDLLE	
HGPRBMY11v1	(38) REEPIVYILVFWCVLGNCSIVFQOPYKKSPEVNMENLAHDLLE	
P2Y5_CHICK	(14) VTHYGEVESVVEVCGVAVVAFITLVVRNEETVYMNLAHDLLE	
P2YR_CHICK	(40) EYVPEIVYILVFLTCFLGNSVAIVMVFHMPWSSSVYMNLAHDLLE	
P2YR_MELGA	(40) EYVPEIVYILVFLTCFLGNSVAIVMVFHMPWSSSVYMNLAHDLLE	
P2YR_RAT	(51) EYVPEIVYILVFLTCFLGNSVAIVMVFHMPWSSSVYMNLAHDLLE	
Q9Y271	(23) NQVYSTLYSMSTVCGFFGNGFVYZVTKTKKSASQVYMNLAHDLLE	
GPRH_HUMAN	(31) NMELASFYVLDFTLAVGNTLALNLEIRDHSGCHPQNVVLAHDLLE	
	101	150
HGPRBMY11	(72) ISTLEFRADYYIRGSNWIFGDIACTMSSEYVNMYSIYFLTVISVVR	
HGPRBMY11v1	(88) ISTLEFRADYYIRGSNWIFGDIACTMSSEYVNMYSIYFLTVISVVR	
P2Y5_CHICK	(64) VETLEFRIIYEVVRN--WFGDVLCKISVTTFYINMYGSILFLTCISVDR	
P2YR_CHICK	(90) VLTLEALIEYYENKIDWIFGDVMCKLQRFIEVNEVGSILFLTCISVHR	
P2YR_MELGA	(90) VLTLEALIEYYENKIDWIFGDVMCKLQRFIEVNEVGSILFLTCISVHR	
P2YR_RAT	(101) VLTLEALIEYYENKIDWIFGDVMCKLQRFIEVNEVGSILFLTCISVHR	
Q9Y271	(73) VCTLEPLRVVYVHKGIMLFGDFLCRSTYAEVNMVCSIEFTMSFFRC	
GPRH_HUMAN	(81) VLVLEPLRLVYHESGNHWPEGETACRLTGFEVNMVASTYFLTCISVDR	
	151	200
HGPRBMY11	(122) LAMVHEPRLHVTISIRSAWILCGEHWILMASSIMCLDS--GSENGSV	
HGPRBMY11v1	(138) LAMVHEPRLHVTISIRSAWILCGEHWILMASSIMCLDS--GSENGSV	
P2Y5_CHICK	(113) LAIVHEPERSKTIRTKRNARIVCAVWITVLACSTIPASFQSTNRQNTTEQ	
P2YR_CHICK	(140) TGVVHELKSLGREKKKNNAVVSSEVVALVVAIAPILEYSGTGVRANKTV	
P2YR_MELGA	(140) TGVVHELKSLGREKKKNNAVVSSEVVALVVAIAPILEYSGTGVRANKTV	
P2YR_RAT	(151) SGVVHELKSLGREKKKNNAVVSSEVVALVVAIAPILEYSGTGVRANKTV	
Q9Y271	(123) IAIIVFVONINLYTOKKAREVCGVGINIEVLTSSPELMAKPQKDEKNNTK	
GPRH_HUMAN	(131) LAIVHEPVKSLKRRPLYAHLACARLVVAVVAMAPLVSPQTVQNTTV	
	201	250
HGPRBMY11	(169) TSCLE--LNLYKHAKEQIMNYIALVVGCLPPEPESITCYLLIIRVLEKVE	
HGPRBMY11v1	(185) TSCLE--LNLYKHAKEQIMNYIALVVGCLPPEPESITCYLLIIRVLEKVE	
P2Y5_CHICK	(163) RTCFENFPSTIKTYISRIISRIETVGFITLQNTYSTVETRLNKPL	
P2YR_CHICK	(190) TCYDT--TADEKRSYFVISMCTVFMFCIPFIVITGCGYGLIVRLIYNE	
P2YR_MELGA	(190) TCYDT--TADEKRSYFVISMCTVFMFCIPFIVITGCGYGLIVRLIYNE	
P2YR_RAT	(201) TCYDS--TSDEKRSYFVISMCTVFMFCIPFIVITGCGYGLIVRLIYNE	
Q9Y271	(173) CFEP--QDNQTKNHLLHYSLVGVFIIPFVILVCTVILLGLKKS	
GPRH_HUMAN	(181) CLQLY-----REKNSHHNYSIAVAFTEPFTTTCYLLIIRSLREG	

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FIG. 6A

1	ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT	60
1	M E R K F M S L Q P S I S V S E M E P N	20
61	GGCACCTTCAGCAATAACAACAGCAGGAAGTGCACAATTGAAAACCTCAAGAGAGAATTT	120
21	G T F S N N N S R N C T I E N F K R E F	40
121	TTCCCAATGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA	180
41	<u>F P I V Y L I I F F W G V L G N G L S I</u>	60
181	TATGTTTTCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTG	240
61	<u>Y V F L</u> Q P Y K K S T S V N <u>V F M L N L</u>	80
241	GCCATTTTCAGATCTCCTGTTTCATAAGCAGCTTCCCTTCAGGGCTGACTATTATCTTAGA	300
81	<u>A I S D L L F I S T L P F R A D Y Y L</u> R	100
301	GGCTCCAATGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC	360
101	G S N W I F G D L A C R I M S Y S L Y <u>V</u>	120
361	AACATGTACAGCAGTATTTATTTCTGACCGTGCTGAGTGTGTGCGTTTCTGGCAATG	420
121	<u>N M Y S S I Y F L T V L S V V R F L A M</u>	140
421	GTCACCCCTTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG	480
141	<u>V H P F R L L H V T S I R S</u> <u>A W I L C G</u>	160
481	ATCATATGGATCCTTATCATGGCTTCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG	540
161	<u>I I W I L I M A S S I M L L</u> D S G S E Q	180
541	AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC	600
181	N G S V T S C L E L N L Y K <u>I A K L Q T</u>	200
601	ATGAACATATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT	660
201	<u>M N Y I A L V V G C L L P F F T L S I C</u>	220
661	TATCTGCTGATCATTCGGGTCTGTAAAGTGGAGGTCCCAGAATCGGGCTGCGGGTT	720
221	<u>Y L L I I R V L L K V E V P E S G L R V</u>	240
721	TCTCACAGGAAGGCACTGACCACCATCATCATCCTTGATCATCTTCTTCTGTGTTTT	780
241	S H R K <u>A L T T I I I T L I I F F L C F</u>	260
781	CTGCCCTATCACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAA	840
261	<u>L P Y H T L</u> R T V H L T T W K V G L C K	280
841	GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC	900
281	D R L H K <u>A L V I T L A L A A A N A C F</u>	300

FIG. 2B

		251		300
HGPRBMY11	(217)	PPESGLRVSHRKA	TTITITLITFF	FLPYH RT L-----TIWK
HGPRBMY11v1	(233)	PPESGLRVSHRKA	TTITITLITFF	FLPYH RT L-----TIWK
P2Y5_CHICK	(213)	ILSRNKLS-KK	KKHHEHVI	FCFEPYP TLI SLMR--TOTWIN
P2YR_CHICK	(238)	EDNSPLR---	RKSITYYIIIVL	TFAVSALPHVITL LRARLDFOTPO
P2YR_MELGA	(238)	EDNSPLR---	RKSITYYIIIVL	TFAVSALPHVITL LRARLDFOTPO
P2YR_RAT	(249)	EDNSPLR---	RKSITYYIIIVL	TFAVSALPHVITL LRARLDFOTPE
Q9Y271	(221)	MKNLSS--HK	KATGIMV	TAAFLVSEMPYHRT LHFLHN--ETKP
GPRH_HUMAN	(224)	RVEERLE---	TKAQRMTAIVL	ATFLVGFMPYHVNR LHYR--HGAS
		301		350
HGPRBMY11	(261)	GLCKDRHKKEL	VITLALAA	ANACFNPLYFFAGLFL RL SALKRGHP
HGPRBMY11v1	(277)	GLCKDRHKKEL	VITLALAA	ANACFNPLYFFAGLFL RL SALKRGHP
P2Y5_CHICK	(260)	CSVVTAMRT	MYPTLCHAVS	NCCFDPIVYFFEDTNS LD --K--V
P2YR_CHICK	(285)	CAFNDKVIAT	YQVTRGLASL	NSCVDPILYFFAGDTFRRLSRATRKSSR
P2YR_MELGA	(285)	CAFNDKVIAT	YQVTRGLASL	NSCVDPILYFFAGDTFRRLSRATRKSSR
P2YR_RAT	(296)	CAFNDKVIAT	YQVTRGLASL	NSCVDPILYFFAGDTFRRLSRATRKSSR
Q9Y271	(267)	CDSVLRMCK	SVVITLSLAAS	NCCFDPILYFFSCGFRRRLS FRKHSL
GPRH_HUMAN	(269)	CATORILAL	ANRITSLTSLN	CAIDPIMYFFVRRFRALNLLCGKRL
		351		379
HGPRBMY11	(311)	KAK-TKCVF	EVS	WLRKEIV-----
HGPRBMY11v1	(327)	KAK-TKCVF	EVS	WLRKEIV-----
P2Y5_CHICK	(306)	QNT-----		
P2YR_CHICK	(335)	SEP-NVQSK	SEEMTINIL	TEYKQNGDTSL
P2YR_MELGA	(335)	SEP-NVQSK	SEEMTINIL	TEYKQNGDTSL
P2YR_RAT	(346)	SEA-NLQSK	SEEMTINIL	SFKQNGDTSL
Q9Y271	(316)	SVT-YVPRK	ASLEK	GEEICKV-----
GPRH_HUMAN	(319)	GPPPSFECK	INSS	SAKSEL-----

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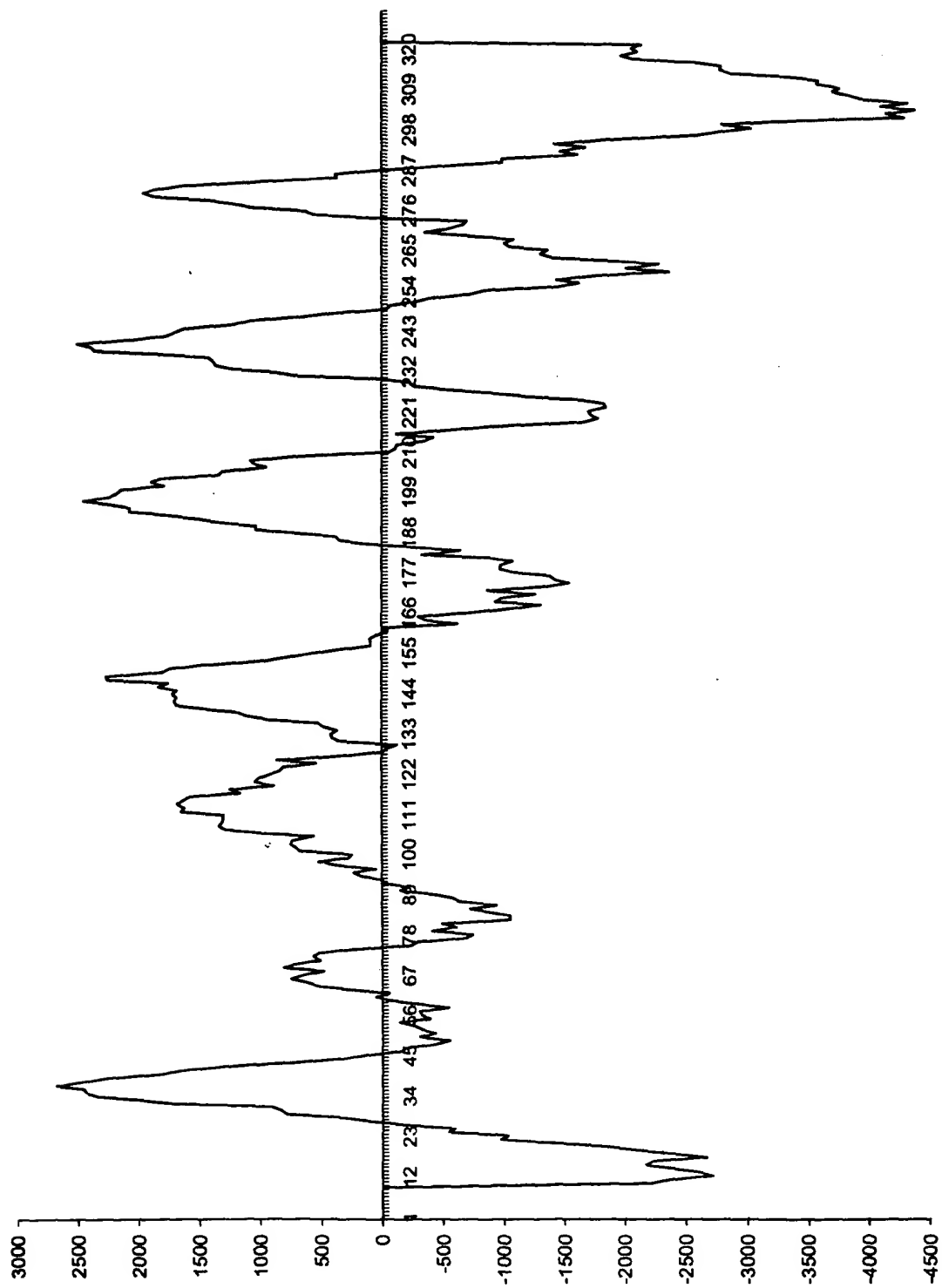


FIG. 3

FIG. 6B

901	AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTC	960
301	<u>N P L L Y Y F A</u> G E N F K D R L K S A L	320
961	AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTCCCTGTTAGTGTGTGGTTG	1020
321	R K G H P Q K A K T K C V F P V S V W L	340
1021	AGAAAGGAAACAAGAGTATAA	1041
341	R K E T R V	346

FIG. 4

Expression Profiling of Novel Human GPCR, HGPRBMY11

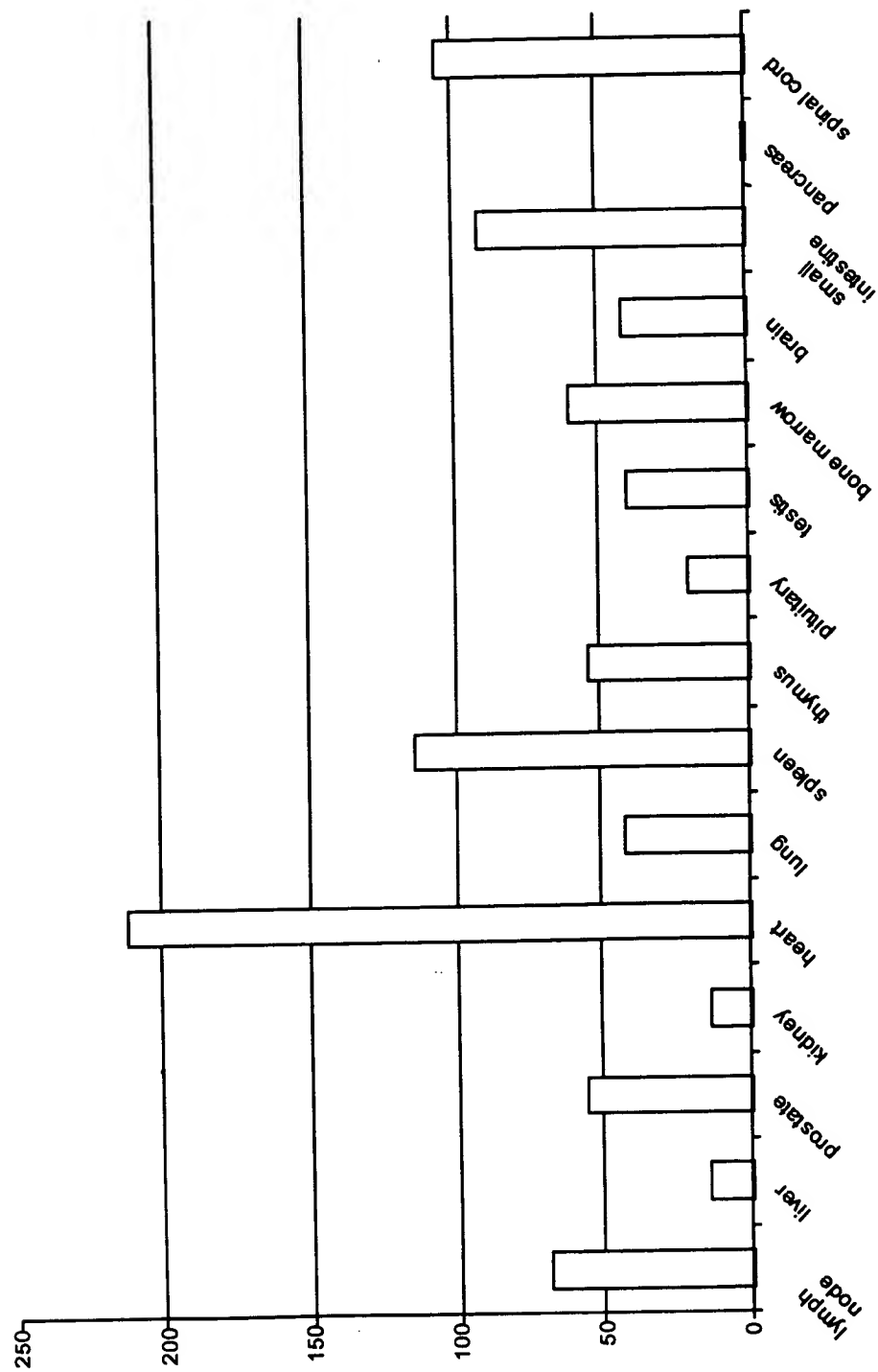


FIG. 5

HGPRBMY11

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37%	49%
chick purinergic receptor 5	gi P32250	36%	46%
human G-protein-coupled receptor GPR17	gi Q13304	36%	46%
chick purinergic receptor	gi P34996	30%	45%
turkey purinergic receptor	gi P49652	30%	45%
rat purinergic receptor	gi P49651	30%	44%

HGPRBMY11v1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37.2%	49%
chick purinergic receptor 5	gi P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi Q13304	36.2%	46.1%
chick purinergic receptor	gi P34996	29.5%	43.9%
turkey purinergic receptor	gi P49652	29.8%	44.2%
rat purinergic receptor	gi P49651	29.6%	44%

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FIG. 7

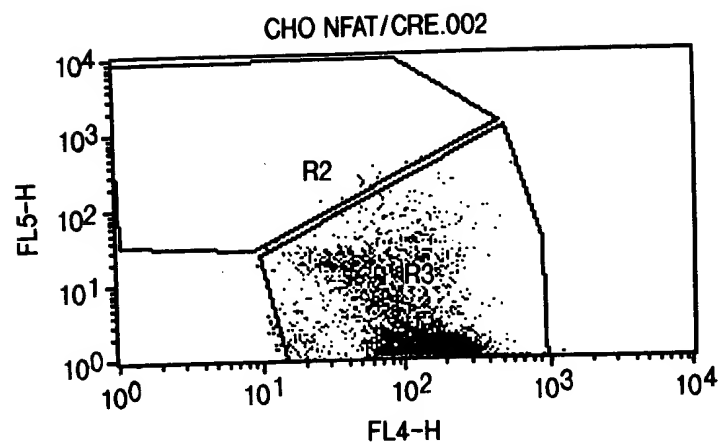


FIG. 8

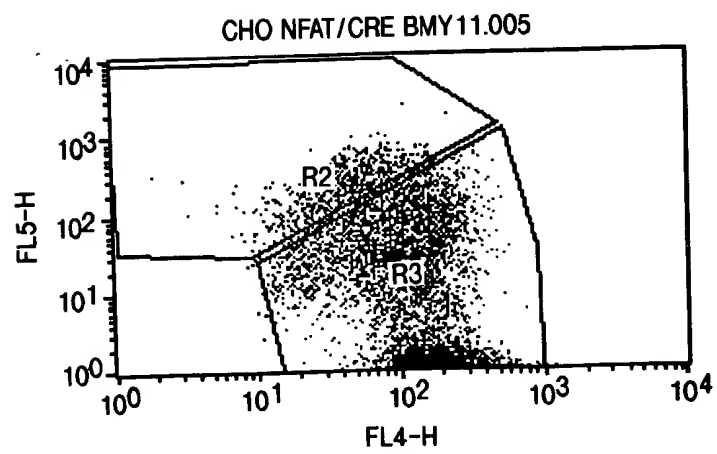


FIG. 9

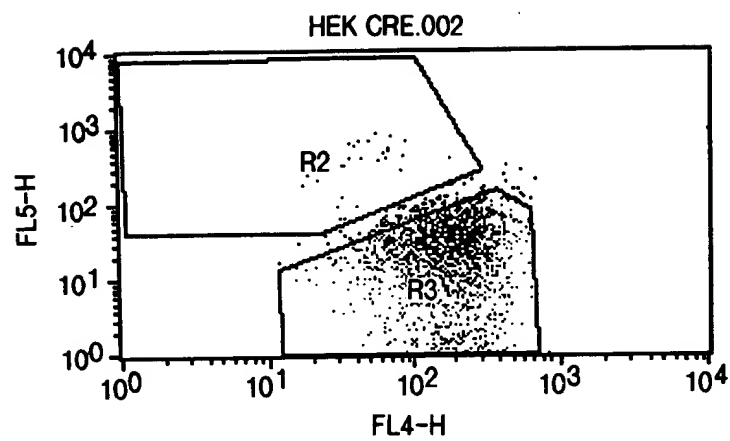
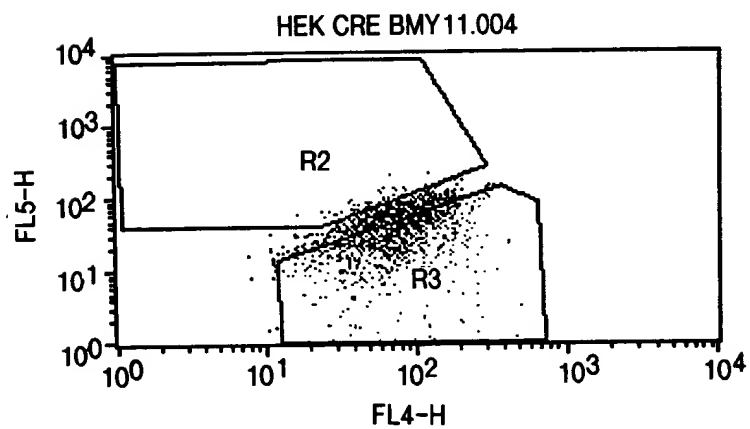


FIG. 10



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FIG. 11

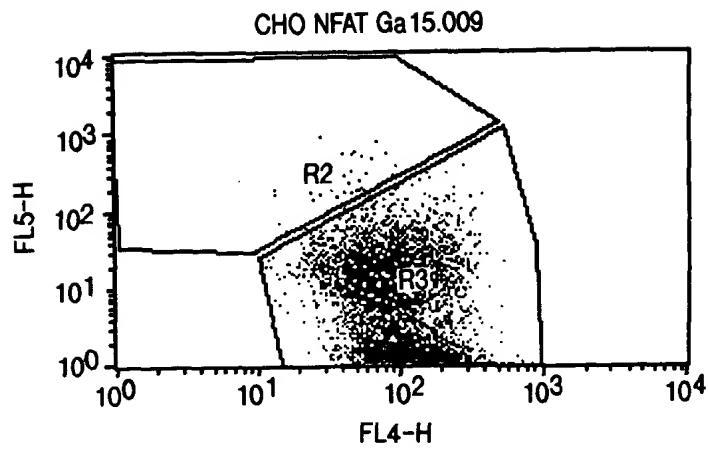


FIG. 12

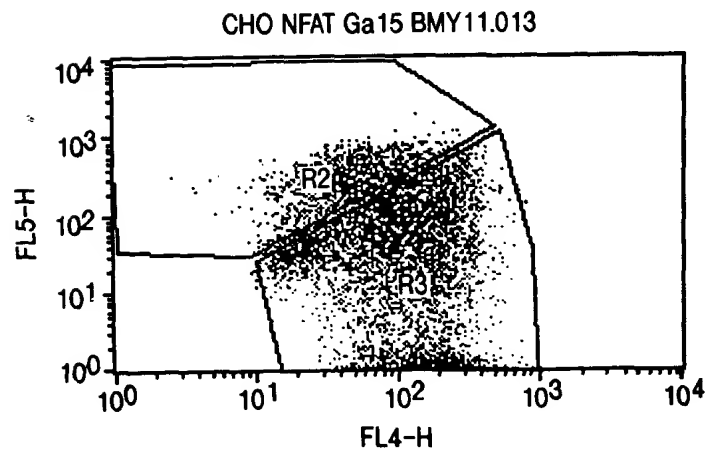


FIG. 13

Cho NFAT Gal5 Control (Fluorescent vs. Bright Field)



Cho NFAT Gal5 BMY11 (Fluorescent vs. Bright Field)

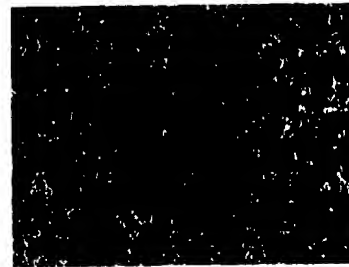
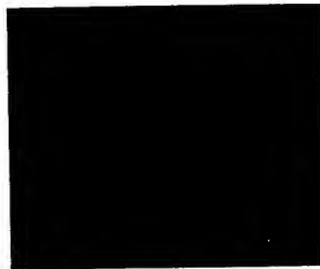


FIG. 14a

Cho-NFAT CRE

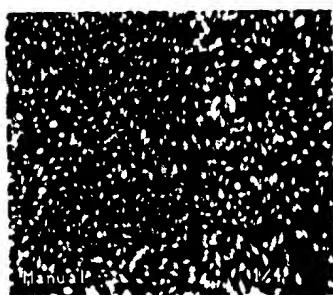


FIG. 14b

Cho-NFAT CRE + F/T/P

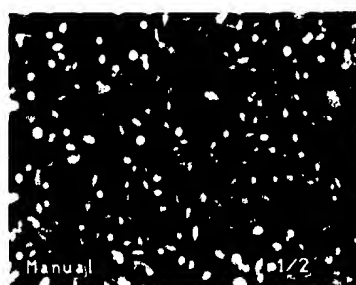


FIG. 14c

Cho-NFAT CRE oGPCR-Intermediate

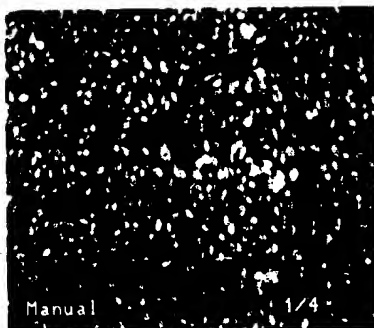


FIG. 14d

Cho-NFAT CRE oGPCR High

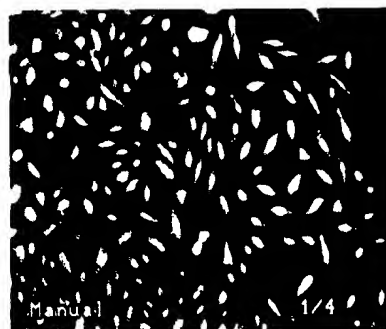


FIG. 15A

1	ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT	60
1	M S L Q P S I S V S E M E P N G T F S N	20
61	AACAACAGCAGGAACTGCACAATTGAAAACCTCAAGAGAGAATTTTCCCAATTGTATAT	120
21	N N S R N C T I E N F K R E F F P I V Y	40
121	CTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTCCTGCAG	180
41	L I I F F W G V L G N G L S I Y V F L Q	60
181	CCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTTCAGATCTC	240
61	P Y K K S T S V N V F M L N L A I S D L	80
241	CTGTTTCATAAGCAGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA	300
81	L F I S T L P F R A D Y Y L R G S N W I	100
301	TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGATGTCAACATGTACAGCAGT	360
101	F G D L A C R I M S Y S L Y V N M Y S S	120
361	ATTTATTTCTGACCGTCTGAGTGTGTGCGTTTCTGGCAATGGTTCACCCCTTTTCGG	420
121	I Y F L T V L S V V R F L A M V H P F R	140
421	CTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT	480
141	L L H V T S I R S A W I L C G I I W I L	160
481	ATCATGGCTTCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTACAC	540
161	I M A S S I M L L D S G S E Q N G S V T	180
541	TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACATATTGCC	600
181	S C L E L N L Y K I A K L Q T M N Y I A	200
601	TTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATT	660
201	L V V G C L L P F F T L S I C Y L L I I	220
661	CGGGTTCTGTAAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA	720
221	R V L L K V E V P E S G L R V S H R K A	240
721	CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTTTCTGCCCCATCACACA	780
241	L T T I I I T L I I F F L C F L P Y H T	260
781	CTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA	840
261	L R T V H L T T W K V G L C K D R L H K	280
841	GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT	900
281	A L V I T L A L A A A N A C F N P L L Y	300

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FIG. 15B

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901 TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA 960
301 Y F A G E N F K D R L K S A L R K G H P 320

961 CAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAGA 1020
321 Q K A K T K C V F P V S V W L R K E T R 340

1021 GTATAA 1026
341 V 341
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